3D $T_2$ mapping of human brain with high accuracy by 3D Turbo-Flash imaging prepared by multiecho adiabatic spin echo

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Introduction

An intrinsic parameter of $T_2$ reflects microscopic characteristics of the in vivo water molecule, such as its mobility and magnetic environment. Thus, $T_2$-weighted imaging is routinely used for diagnosing various diseases. In contrast, quantitative $T_2$ mapping has been pursued to a limited extent, due in part to obstacles in obtaining accurate $T_2$ values with slice-selective spin-echo sequences. In particular, imperfections in the slice profile produced by the refocusing pulse result in a loss of coherence, and when multiple echoes are collected the loss is cumulative at each refocusing step, leading to erroneous $T_2$ estimations. Although $T_2$ measurements by stepping TE values in a single spin-echo sequence can avoid that cumulative error, other mechanisms of loss of phase coherence occurs during the long TE periods due to diffusion in nonuniform $B_0$ and exchange of the water molecule. At higher fields these two types of effects are exacerbated by increased $B_1$ inhomogeneity and larger microscopic susceptibility gradients. To overcome these problems, we have proposed the single slice multiecho adiabatic spin echo (MASE) imaging sequence. In this method, accurate $T_2$ maps can be obtained by a pair of adiabatic full passage (AFP) pulses having a feature of very precise slice selection. Through measuring a $T_2$ map of the slice across the basal ganglia region of human brain with high accuracy using this method, we have found that the transverse relaxation rate ($1/T_2$) of the tissue water in human brain at 4.7 T has a high linear correlation with the published levels of non-haem iron content (1, 2). Shortening measurement time is a key for expanding this single slice method (2D MASE) into 3D $T_2$ mapping. In this work, we propose 3D MASE method of whole brain $T_2$ mapping by 3D Turbo-Flash imaging prepared by MASE module. This method has features of accurate $T_2$ mapping using adiabatic pulses and of fast imaging by 3D Turbo-Flash.

Materials and Method

Figure 1 shows our proposed 3D MASE imaging sequence for whole brain $T_2$ mapping. In the MASE module, magnetization decayed by $T_2$ without a loss of coherence can be generated by a multi-pulse spin echo sequence consisting of an adiabatic half-passage (AHP) and series of a pair of AFP pulses. This transverse magnetization is flipped back to the longitudinal magnetization by a flipback AHP pulse. After crusher gradient pulses are applied to eliminate residual transverse magnetization, signal is accumulated by 3D Turbo-Flash imaging module. For 3D $T_2$ mapping, multiple 3D images with different TE values by adding a pair of AHP pulses in the MASE module are collected. The case of a value of 2TE is shown in Fig. 1. To maintain constant magnetization recovered by $T_1$ every segment, an AHP pulse for the saturation recovery is applied before the MASE module. Signal intensity in the 3D image with $n$TE by this sequence can be described as $S(nTE) = (1-e^{-nRD/T_2})e^{nTE/T_2}$. After collecting multiple 3D images, $T_2$ maps are calculated by fitting the signal intensity of each pixel in the 3D images using that model equation of signal intensity.

All the measurements were performed on a 4.7 T whole-body MRI system (INOVA, Agilent) using a quadrature TEM head coil. For validation, $T_2$ measurements of a spherical phantom containing agarose gel with $T_1$ of 1.1 s and $T_2$ of 92 ms were performed by the 3D MASE method. In human brain measurements, three whole brain 3D images with TE = 26, 52, 78 ms were collected. In the turbo-Flash imaging module, TR/TE = 8.1/2.6 ms and flip angle is 15 degrees. An imaging matrix is $256 \times 96 \times 96$ along y (read), z (slice and phase1) and x (phase2) directions with FOV of $256 \times 240 \times 192$ mm$^3$, giving a spatial resolution of $1 \times 2.5 \times 2$ mm$^3$. MR signals were accumulated by centric phase-encoding order with number of segments of 2 along the z direction. The relaxation delay was set to 3 s. Each 3D image was collected for 11 min, resulting 33 min for the total measurement time. $T_2$ values in several regions in gray and white matters (GM, WM) on the slice across the basal ganglia region were compared to $T_2$ values measured by the 2D MASE.

Results & Discussion

$T_2$ of the gel phantom measured by 3D MASE was 90.1 ms ± 3.1 ms, which was in good agreement with $T_2$ of 92 ms measured by the conventional method. Figure 2 shows a whole brain $T_2$ map measured by 3D MASE sequence. $T_2$ values of the tissue in GM and WM regions measured by 3D MASE were in good agreement with those by the 2D MASE (Fig. 3).

Conclusions

We successfully implemented 3D MASE method to allow whole brain $T_2$ mapping with high accuracy.

References


![Fig. 1. 3D MASE imaging sequence for whole brain $T_2$ mapping. The case of echo time = 2TE is shown. RD: relaxation delay.](image1)

![Fig. 2. A $T_2$ map of whole human brain measured by the proposed 3D MASE imaging sequence.](image2)

![Fig. 3. Correlation of $T_2$ values measured by 3D MASE with those by 2D MASE.](image3)